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QUE PYRUVATE DECARBOXYLASE

FILE 'CAPLUS, BIOSIS, SCISEARCH, MEDLINE, EMBASE, BIOTECHNO, LIFESCI, PASCAL, DGENE, ESBIODASE, BIOTECHDS' ENTERED AT 17:26:10 ON 24 APR 2003

L1

L2 52 S L1 AND THERMOSTAB?
L3 457722 S L2 AND YEAST OR SACCHARO?
L4 27 S L2 AND (YEAST OR SACCHARO?)
L5 10 DUP REM L4 (17 DUPLICATES REMOVED)
L6 116 S L1 AND (PDC5 OR PDC 5)
L7 114 S L6 AND (GENE OR CDNA OR CLON?)
L8 28 DUP REM L7 (86 DUPLICATES REMOVED)
L9 0 S L8 AND THERMOST?
L10 0 S L8 AND (OPTIM? TEMP?)
L11 2 S L8 AND TEMP?

=> log Y

L5 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1979:401925 CAPLUS

DOCUMENT NUMBER: 91:1925

TITLE: The effects of the chemical surface structures of functionalized polystyrenes on the kinetic properties of immobilized **yeast pyruvate decarboxylase**

AUTHOR(S): Beitz, J.; Schellenberger, A.

CORPORATE SOURCE: Sekt. Biowiss., Martin-Luther-Univ. Halle-Wittenberg, Halle/Saale, 402, Ger. Dem. Rep.

SOURCE: Acta Biologica et Medica Germanica (1979), 37(9), 1399-411
CODEN: ABMGAJ; ISSN: 0001-5318

DOCUMENT TYPE: Journal

LANGUAGE: German

AB The influence of the loading d. of different functional groups and the length of suitable spacer structures on the kinetic properties of **yeast pyruvate decarboxylase** were investigated on identical polystyrene matrixes. At const. concns. of the fixed protein, both the specific activity and the storage stability of the immobilized enzymes increased with increasing concns. of the protein-binding C:O groups. The pH optimum and Km value were functions of the NH₃⁺-content of the supports. Using 4 spacer resins with an equal content of spacer groups, it could be shown that the optimum time of coupling as well as the max. catalytic activity, storage stability, and **thermostability** depend on the length of the spacer structures. On the other hand, the mobility of an ESR marker fixed via the same spacers to the resin was not affected by the different spacer structures.

ACCESSION NUMBER: 1999:436880 CAPLUS

DOCUMENT NUMBER: 131:210818

TITLE: Effects of substitution of tryptophan 412 in the substrate activation pathway of yeast **pyruvate decarboxylase**

AUTHOR(S): Li, Haijuan; Jordan, Frank

CORPORATE SOURCE: Departments of Chemistry and Biological Sciences and Program in Cellular and Molecular Biodynamics, Rutgers the State University, Newark, NJ, 07102, USA

SOURCE: Biochemistry (1999), 38(31), 10004-10012

CODEN: BICHAW; ISSN: 0006-2960

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Oligonucleotide-directed site-specific mutagenesis was carried out on **pyruvate decarboxylase** (EC 4.1.1.1) from *Saccharomyces cerevisiae* at Trp-W412, located on the putative substrate activation pathway and linking Glu-91 on the .alpha. domain with Trp-412 on the .gamma. domain of the enzyme. Whereas Cys-221 on the .beta. domain is the residue at which substrate activation is triggered, that information, via the substrate bound at Cys-221, is transmitted to His-92 on the .alpha. domain, across the domain divide from Cys-221, thence to Glu-91 on the .alpha. domain, and then on to Trp-412 on the .gamma. domain and to the active site thiamin diphosphate (ThDP) located at the interface of the .alpha. and .gamma. domains. Here, substitution at Trp-412 with Phe and Ala was carried out, resulting in active enzymes with specific activities about 4- and 10-fold lower than that of the wild-type enzyme. Even though Trp-412 interacted with Glu-91 and His-115 via a main chain H-bond donor and acceptor, resp., there was clear evidence for the importance of the indole side-chain of Trp-412 from a variety of expts.: **thermostability**, fluorescence quenching, the binding consts. of ThDP, and CD spectroscopy, in addn. to conventional steady-state kinetic measurements. Whereas the substrate activation was still prominent in the W412F variant, its level was very much reduced in the W412A variant, signaling that the size of the side-chain was also important in positioning the amino acids surrounding the active center to achieve substrate activation. The fluorescence studies demonstrated that Trp-412 is a relatively minor contributor to the well-documented fluorescence of apopyruvate decarboxylase in its native state. The information about the Trp-412 variants provided strong addnl. support for the putative substrate activation pathway from Cys-221 .fwdarw. His-92 .fwdarw. Glu-91 .fwdarw. Trp-412 .fwdarw. Gly-413 .fwdarw. ThDP. The accumulating evidence for the central role of the .beta. domain in stabilizing the overall structure was summarized.

ACCESSION NUMBER: 1990:453406 CAPLUS

DOCUMENT NUMBER: 113:53406

TITLE: Autoregulation may control the expression of yeast

pyruvate decarboxylase structural
genes PDC1 and PDC5

AUTHOR(S): Hohmann, Stefan; Cederberg, Hakan

CORPORATE SOURCE: Inst. Mikrobiol., TH Darmstadt, Darmstadt, D-6100,
GermanySOURCE: European Journal of Biochemistry (1990), 188(3),
615-21

CODEN: EJBCAI; ISSN: 0014-2956

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The authors deleted the **pyruvate decarboxylase** structural **gene PDC1** from the genome of *Saccharomyces cerevisiae*. The *pdcl* deletion mutants had **pyruvate decarboxylase** activity due to the presence of a second structural **gene**. This **gene, PDC5**, was cloned and sequenced. The predicted amino acid sequences of **PDC1** and **PDC5** are 88% identical. Deletion of **PDC5** did not cause any decrease in the specific **pyruvate decarboxylase** activity, while *pdcl* deletion mutants had 80% of the wild-type activity. Deletion mutants lacking both **PDC1** and **PDC5** did not show any detectable **pyruvate decarboxylase** activity in vitro and were unable to ferment glucose. This indicates that **PDC1** and **PDC5** are the only structural **genes** for **pyruvate decarboxylase** in yeast. The **PDC5** isoenzyme showed a slightly higher K_m value for its substrate pyruvate than the **PDC1** product (**PDC5**: $K_m = 8$ mM; **PDC1**: $K_m = 5$ mM), as measured in a crude ext. of *pdcl* and *pdcl5* deletion mutants, resp. **PDC5** is only expressed in *pdcl* deletion mutants. No mRNA transcribed from **PDC5** could be detected in wild-type cells. Thus, in addn. to the control by glucose induction, **pyruvate decarboxylase** activity seems to be subject to autoregulation. Similar phenomena have been described previously for tubulin, histones, and a ribosomal protein but not for metabolic enzymes.

L8 ANSWER 21 OF 28 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1993:161969 CAPLUS

DOCUMENT NUMBER: 118:161969

TITLE: Structure and expression of yeast **pyruvate decarboxylase** structural **genes**

AUTHOR(S): Hohmann, Stefan

CORPORATE SOURCE: Inst. Mikrobiol., Tech. Hochsch. Darmstadt, Darmstadt, D-6100, Germany

SOURCE: Biochem. Physiol. Thiamin Diphosphate Enzymes, Proc. Int. Meet. Funct. Thiamin Diphosphate Enzymes (1991), Meeting Date 1990, 106-14. Editor(s): Bisswanger, Hans; Ullrich, Johannes. VCH: Weinheim, Fed. Rep. Ger.

CODEN: 57LOA7

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Three structural **genes** for pyruvate tdecarboxylase named PDC1, PDC5, and PDC6 have been identified in the haploid genome of *Saccharomyces cerevisiae* and the DNA sequences of these **genes** have been detd. All three **genes** code for primary translation products of 563 amino acids and the deduced amino acid sequences are 88% (PDC1-PDC5), 83% (PDC1-PDC6), 80% (PDC5-PDC6) and 78% (PDC1-PDC5-PDC6) identical. The differences in the primary structure are unevenly distributed over the protein sequence. The three structural **genes** are differentially expressed. In wild-type yeast strains growing on glucose, the product of PDC1 is at least six times more abundant than the PDC5 product. Deletion mutants lacking both the PDC1 and the PDC5 **gene** have no detectable **pyruvate decarboxylase** activity in crude exts. This indicates that the third structural **gene**, PDC6, is not expressed during growth on glucose. However, expression of PDC6 was obsd. in certain mutants where PDC6 had come under the control of the PDC1 promoter by a spontaneous rearrangement. In mutants where the PDC1 **gene** has been deleted, the expression of PDC5 is enhanced between 4-5 fold, apparently to compensate for the loss of the PDC1 structural **gene**. This phenomenon points to an involvement of **pyruvate decarboxylase** in the regulation of its own synthesis.

L5 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1995:937941 CAPLUS

DOCUMENT NUMBER: 124:3896

TITLE: The enzyme properties of **pyruvate decarboxylase** modified with an amylose derivative

AUTHOR(S): Ohba, Hideki; Yasuda, Seiji; Hirose, Hideharu; Yamasaki, Nobuyuki

CORPORATE SOURCE: Mater. Chem. Dep., Kyushu Natl. Ind. Res. Inst., Tosu, 841, Japan

SOURCE: Kyushu Kogyo Gijutsu Kenkyusho Hokoku (1995), 55, 3423-30

CODEN: KKOHE5; ISSN: 1340-3958

PUBLISHER: Kyushu Kogyo Gijutsu Kenkyusho

DOCUMENT TYPE: Journal

LANGUAGE: English

AB An amylose-glycylglycine adduct (AG) was covalently attached to **pyruvate decarboxylase** (PyDC) from brewer's **yeast**, and some properties of the resulting conjugate (AG-PyDC) were studied with regard to **thermostability**. The conjugate was prep'd. by modification of PyDC with the N-hydroxysuccinimide ester of AG (AG-ONSu), and purified by gel filtration on a Bio gel P-199 column. Anal. data indicated that in the conjugate, 30 out of 68 amino groups in the PyDC mol. were modified with AG-ONSu and the main chain configuration of PyDC remained unchanged. By conjugation with AG the optimum temp. of the activity of PyDC changed from 35.degree. to 40.degree. The conjugate showed a greater resistance than PyDC to inactivation by heat treatment: after treatment of the samples at 45.degree. for 20 min, AG-PyDC retained 80% of the activity, while the activity of native PyDC was only 25% of that of the untreated sample. It is suggested that AG-ONSu can be advantageously used for stabilization of the thermolabile enzyme, PyDC.

L6 ANSWER 4 OF 7 BIOTECHDS COPYRIGHT 2003 THOMSON DERWENT AND ISI

ACCESSION NUMBER: 2001-16051 BIOTECHDS

TITLE: Gram-positive bacteria for producing ethanol are transformed with a heterologous gene encoding pyruvate-decarboxylase or a functional equivalent and have solely **native alcohol-dehydrogenase** function;

plasmid pFC1-mediated *Zymomonas mobilis* or *Saccharomyces cerevisiae* enzyme gene transfer and expression in *Bacillus* sp. and L-lactic acid production

AUTHOR: Green E; Baghaei-Yazdi N; Javed M

PATENT ASSIGNEE: Elsworth-Biotechnology

LOCATION: Surrey, UK.

PATENT INFO: WO 2001049865 12 Jul 2001

APPLICATION INFO: WO 2001-GB36 5 Jan 2001

PRIORITY INFO: US 2000-177199 21 Jan 2000; GB 2000-185 6 Jan 2000

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: WPI: 2001-496722 [54]

AB A Gram-positive bacterium (I, **Bacillus** *stearothermophilus*, **Bacillus** *calvodox*, **Bacillus** *caldotenax*, **Bacillus** *thermoglucosidasius*, **Bacillus** *coagulans*, **Bacillus** *thermodenitrificans* and **Bacillus** *caldolyticus*) transformed with a gene encoding *Zymomonas mobilis* or *Saccharomyces cerevisiae* pyruvate-decarboxylase (pdc, EC-4.1.1.1), with 300 bp DNA sequence fully defined, or a functional equivalent is claimed. Also claimed are: a method for producing ethanol; a method for producing L-lactic acid; a nucleic acid molecule containing the lactate-dehydrogenase promoter region of strain LN (NCIMB-41038); and plasmid pFC1. In an example, plasmid pFC1-PDC1 was transformed into *Bacillus* sp. TN and cultured in culture medium containing JSD supplemented with 50 mM PIPES buffer and 2% glucose at 54 deg for 24 hr. The TN-P3 strain was shown to produce 39.5 mM ethanol. The above can be used for producing ethanol and at high temp. and for producing L-lactic acid. (30pp)